



METACORE

— INTEGRATED PATHWAY ANALYSIS FOR MULTI-OMICS DATA

GAIN GREATER INSIGHT INTO DISEASE UNDERSTANDING

MetaCore™ delivers high-quality biological systems content in context, giving you essential data and analytics to accelerate your scientific research.

INTEGRATED PATHWAY ANALYSIS FOR MULTI-OMICS DATA

MetaCore is an integrated software suite for functional analysis of Next Generation Sequencing, microarray, metabolic, proteomics, siRNA, microRNA, and screening data. MetaCore is based on a high-quality, manually curated database of:

- Transcription factors, receptors, ligands, kinases, drugs, and endogenous metabolites, as well as other molecular classes
- Species-specific directional interactions between protein-protein, protein-DNA and protein-RNA interactions, drug targeting, and bioactive molecules and their effects
- Signaling and metabolic pathways represented on maps and networks
- Rich ontologies for diseases and processes with hierarchical or graphic output

USE METACORE FOR

- Pathway analysis of omics data for drug discovery
- Overlay of public information to enhance interpretation and accuracy
- Knowledge mining of the database for hypothesis generation

- Target and biomarker identification and validation
- Disease pathway modeling and investigation of causal mechanisms
- Patient stratification and mechanism of action (MoA) reconstruction

WHO CAN BENEFIT

- Biological researchers
- Discovery biologists
- Bioinformaticians
- Biomarker groups and preclinical researchers
- Heads of therapy area
- Principal investigators
- Translational researchers

TRUSTED CONTENT

The data contained within MetaCore is industry leading in accuracy, reliability, and comprehensiveness, manually curated by PhD- and MD-level research professionals. There are more than a million small-scale experiment interactions, defined with directionality, effect, and mechanism, and supported by literature for ease of reference.

SEIZE THE OPPORTUNITY NEXT-GENERATION SEQUENCING (NGS) PRESENTS IN IMPROVING DISEASE UNDERSTANDING

Our extended DNA NGS capability is fully integrated with MetaCore. The Genomic Analysis tools help you identify potentially significant variants with 27 filters, including functional predictions, conservation scores, population frequencies, and biological and clinical evidence.

- Embedded workflows for combining VCF variant files with other omics data
- Easy-to-use comprehensive filters to build up complex queries to identify variants of significance, integrated with 1000 Genomes and Exome Sequencing Project (ESP) data
- Trusted, manually annotated gene variant associations in the context of human health, rigorously controlled for quality
- Gene variant content is extracted from global patents and conferences, as well as from clinically actionable sources such as published clinical trial registries, multiple clinical guidelines, and approval documents from FDA, EMA, and Japan
- Workflows for defining Cochran-Armitage Trend Test significance in a cohort analysis, Somatic Mutations, and inheritance patterns in a trio analysis

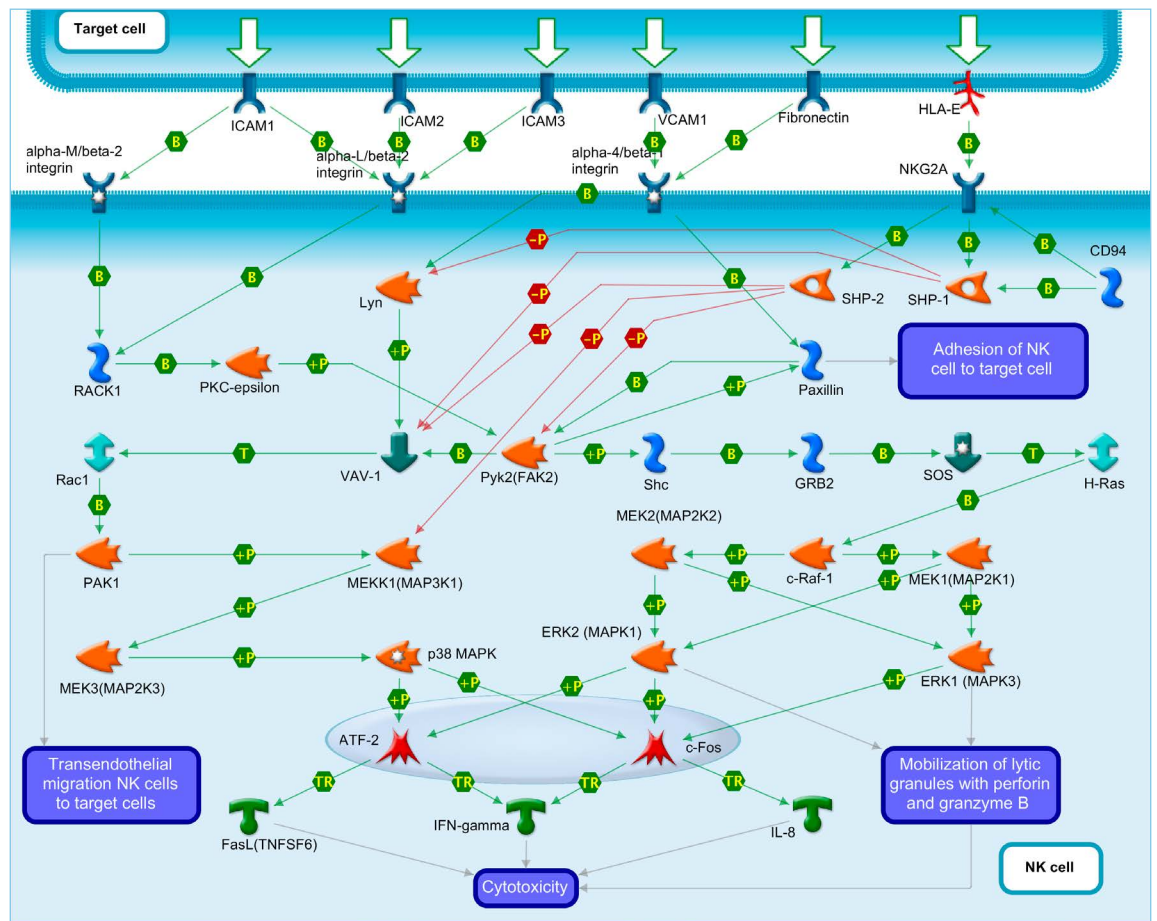
METACORE HIGHLIGHTS

- Integrated analysis of gene expression and gene variant data with copy number, microarray, metabolic, proteomics, siRNA, microRNA, and screening data
- Industry-leading advanced analytics, such as overconnectivity and causal reasoning algorithms, for identifying key hubs and pathways associated with your data
- More than 1.6 million trusted, manually annotated molecular interactions, rigorously controlled for quality from human, mouse, and rat small-scale experiments
- More than 1,600 Pathway Maps, including more than 700 disease-specific maps

TECH SPECS

Web browser

- Internet Explorer® version 9.0
- Firefox® 17
- Safari® 6 or higher
- Chrome 33
- Macromedia Flash Player 8 or higher
- Java Runtime Environment (JRE) 1.5.0



Example of a MetaCore canonical pathway map showing “the role of integrins in Natural Killer (NK) cell cytotoxicity” in immune response. Pathway maps in MetaCore are manually reconstructed by our experts based on findings from peer-reviewed literature references and are fully interactive.

- Save time on literature research (some pathway maps represent a collection of over 300 references)
- Overlay your own experimental data to visualize results and generate actionable hypotheses

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